

TH



PCT10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/088,744

DATE: 08/13/2002  
TIME: 16:40:25

Input Set : A:\Igs4n21.app  
Output Set: N:\CRF4\08132002\J088744.raw

3 <110> APPLICANT: SOLVAY PHARMACEUTICALS B.V.  
5 <120> TITLE OF INVENTION: Novel human G-protein coupled Receptor  
7 <130> FILE REFERENCE: SPW99.06/HA 00.19  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/088,744  
C--> 10 <141> CURRENT FILING DATE: 2002-07-22  
12 <160> NUMBER OF SEQ ID NOS: 34  
14 <170> SOFTWARE: PatentIn Ver. 2.1  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 1658  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Homo sapiens  
21 <220> FEATURE:  
22 <221> NAME/KEY: CDS  
23 <222> LOCATION: (55)..(1299)  
24 <223> OTHER INFORMATION: IGS4A long version  
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28 Met  
29 1  
31 tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa 105  
32 Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys  
33 5 10 15  
35 cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg 153  
36 Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu  
37 20 25 30  
39 gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct 201  
40 Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser  
41 35 40 45  
43 gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg 249  
44 Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu  
45 50 55 60 65  
47 gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac 297  
48 Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn  
49 70 75 80  
51 tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt 345  
52 Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
53 85 90 95  
55 gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg 393  
56 Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu  
57 100 105 110  
59 ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg 441  
60 Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val  
61 115 120 125

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63	tgc	ttc	gcc	tcc	atc	ctc	agc	atc	acc	acc	gtc	agc	gtg	gag	cgc	tac	489
64	Cys	Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	
65	130				135				140					145			
67	gtg	gcc	atc	cta	cac	ccg	ttc	cgc	gcc	aaa	ctg	cag	agc	acc	cgg	cgc	537
68	Val	Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	
69					150				155					160			
71	cgg	gcc	ctc	agg	atc	ctc	ggc	atc	gtc	tgg	ggc	ttc	tcc	gtg	ctc	ttc	585
72	Arg	Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	
73					165				170					175			
75	tcc	ctg	ccc	aac	acc	agc	atc	cat	ggc	atc	aag	ttc	cac	tac	ttc	ccc	633
76	Ser	Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	
77					180				185					190			
79	aat	ggg	tcc	ctg	gtc	cca	ggt	tcg	gcc	acc	tgt	acg	gtc	atc	aag	ccc	681
80	Asn	Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	
81					195				200					205			
83	atg	tgg	atc	tac	aat	ttc	atc	atc	cag	gtc	acc	tcc	ttc	ctg	ttc	tac	729
84	Met	Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	
85					210				215					220		225	
87	ctc	ctc	ccc	atg	act	gtc	atc	agt	gtc	ctc	tac	tac	tac	ctc	atg	gca	777
88	Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	
89					230				235					240			
91	aga	cta	aag	aaa	gac	aaa	tct	ctt	gag	gca	gat	gaa	ggg	aat	gca	aat	825
92	Arg	Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	
93					245				250					255			
95	att	caa	aga	ccc	tgc	aga	aaa	tca	gtc	aac	aag	atg	ctg	ttt	gtc	ttg	873
96	Ile	Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	Leu	
97					260				265					270			
99	gtc	tta	gtg	ttt	gct	atc	tgt	tgg	gcc	ccg	ttc	cac	att	gac	cga	ctc	921
100	Val	Leu	Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	Leu	
101					275				280					285			
103	ttc	ttc	agc	ttt	gtg	gag	gag	tgg	agt	gaa	tcc	ctg	gct	gct	gtg	ttc	969
104	Phe	Phe	Ser	Phe	Val	Glu	Glu	Trp	Ser	Glu	Ser	Leu	Ala	Ala	Val	Phe	
105					290				295					300		305	
107	aac	ctc	gtc	cat	gtg	gtg	tca	ggt	gtc	ttc	tac	ctg	agt	tca	gct		1017
108	Asn	Leu	Val	His	Val	Val	Ser	Gly	Val	Phe	Phe	Tyr	Leu	Ser	Ser	Ala	
109					310				315					320			
111	gtc	aac	ccc	att	atc	tat	aac	cta	ctg	tct	cgc	cgc	ttc	cag	gca	gca	1065
112	Val	Asn	Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala	Ala	
113					325				330					335			
115	ttc	cag	aat	gtg	atc	tct	tct	ttc	cac	aaa	cag	tgg	cac	tcc	cag	cat	1113
116	Phe	Gln	Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln	His	
117					340				345					350			
119	gac	cca	cag	ttg	cca	cct	gcc	cag	cg	aac	atc	ttc	ctg	aca	gaa	tgc	1161
120	Asp	Pro	Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu	Cys	
121					355				360					365			
123	cac	ttt	gtg	gag	ctg	acc	gaa	gat	ata	ggt	ccc	caa	ttc	cca	tgt	cag	1209
124	His	Phe	Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Pro	Cys	Gln	
125					370				375					380		385	
127	tca	tcc	atg	cac	aac	tct	cac	cca	aca	gcc	ctc	tct	agt	gaa	cag		1257

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128 Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln  
129 390 395 400  
131 atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc 1299  
132 Met Ser Arg Thr Asn Tyr Gln Ser Phe His Asn Lys Thr  
133 405 410 415  
135 tgaattcttt cagagctgac tctcctctat gcctcaaaac ttccagaggg aacatcccat 1359  
137 aatgtatgcc ttctcatatg atattagaga ggtagaatgg ctcttacaac tcattgtaccc 1419  
139 attgctagtt tttttttt aataaacgtg aaaactgaga gtttagatctg gtttcaaaac 1479  
141 ccaagactgc ctgattttta gttatcttc cactatccta actgcctcat gccccttcac 1539  
143 tagttcatgc caagaacgtg actggaaagg catggcacct ataccttcat taatttccat 1599  
145 taatggaaat ggttcgtcct gagtcatcta cggtccgagt caggctgtca ctctacta 1658  
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150 <212> TYPE: PRT  
151 <213> ORGANISM: Homo sapiens  
153 <400> SEQUENCE: 2  
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155 1 5 10 15  
157 Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr  
158 20 25 30  
160 Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
161 35 40 45  
163 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
164 50 55 60  
166 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
167 65 70 75 80  
169 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
170 85 90 95  
172 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
173 100 105 110  
175 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
176 115 120 125  
178 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
179 130 135 140  
181 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
182 145 150 155 160  
184 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu  
185 165 170 175  
187 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe  
188 180 185 190  
190 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys  
191 195 200 205  
193 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe  
194 210 215 220  
196 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala  
197 225 230 235 240  
199 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala  
200 245 250 255  
202 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val

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203	260	265	270	
205	Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg			
206	275	280	285	
208	Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val			
209	290	295	300	
211	Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser			
212	305	310	315	320
214	Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala			
215	325	330	335	
217	Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln			
218	340	345	350	
220	His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu			
221	355	360	365	
223	Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys			
224	370	375	380	
226	Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu			
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234	<210> SEQ ID NO: 3			
235	<211> LENGTH: 1658			
236	<212> TYPE: DNA			
237	<213> ORGANISM: Homo sapiens			
239	<220> FEATURE:			
240	<221> NAME/KEY: CDS			
241	<222> LOCATION: (64)..(1299)			
242	<223> OTHER INFORMATION: IGS4A short version			
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247	ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108			
248	Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu			
249	1 5 10 15			
251	gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156			
252	Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala			
253	20 25 30			
255	tcc ctc tgc gga cct cgg cgc agc cac ttc ctc ccc gtg tct gtg 204			
256	Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val			
257	35 40 45			
259	gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252			
260	Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val			
261	50 55 60			
263	tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300			
264	Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr			
265	65 70 75			
267	tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348			
268	Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Gly			
269	80 85 90 95			
271	atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396			
272	Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe			

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273	100	105	110	
275	ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtc tgc			444
276	Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys			
277	115	120	125	
279	ttc gcc tcc atc ctc agc atc acc acc gtc agc gtc gag cgc tac gtc			492
280	Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val			
281	130	135	140	
283	gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg			540
284	Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg			
285	145	150	155	
287	gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtc ctc ttc tcc			588
288	Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser			
289	160	165	170	175
291	ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat			636
292	Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn			
293	180	185	190	
295	ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc atg			684
296	Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met			
297	195	200	205	
299	tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc			732
300	Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu			
301	210	215	220	
303	ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga			780
304	Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg			
305	225	230	235	
307	cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att			828
308	Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile			
309	240	245	250	255
311	caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc			876
312	Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val			
313	260	265	270	
315	tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc			924
316	Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe			
317	275	280	285	
319	ttc agc ttt gtg gag gag tgg agt gaa tcc ctg gct gct gtg ttc aac			972
320	Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val Phe Asn			
321	290	295	300	
323	ctc gtc cat gtg gtg tca ggt gtc ttc ttc tac ctg agc tca gct gtc			1020
324	Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser Ala Val			
325	305	310	315	
327	aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc			1068
328	Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe			
329	320	325	330	335
331	cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac			
332	Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp			
333	340	345	350	
335	cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac			1164
336	Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His			
337	355	360	365	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/13/2002  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 21,24  
Seq#:14; N Pos. 22,25,28